

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:SSPTASXS1656

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * Welcome to STN International * * * * *
* *

NEWS	1		Web Page URLs for STN Seminar Schedule - N. America
NEWS	2		"Ask CAS" for self-help around the clock
NEWS	3	DEC 18	CA/CAPlus pre-1967 chemical substance index entries enhanced
			with preparation role
NEWS	4	DEC 18	CA/CAPlus patent kind codes updated
NEWS	5	DEC 18	MARPAT to CA/CAPlus accession number crossover limit increased
			to 50,000
NEWS	6	DEC 18	MEDLINE updated in preparation for 2007 reload
NEWS	7	DEC 27	CA/CAPlus enhanced with more pre-1907 records
NEWS	8	JAN 08	CHEMLIST enhanced with New Zealand Inventory of Chemicals
NEWS	9	JAN 16	CA/CAPlus Company Name Thesaurus enhanced and reloaded
NEWS	10	JAN 16	IPC version 2007.01 thesaurus available on STN
NEWS	11	JAN 16	WPIDS/WPINDEX/WPIX enhanced with IPC 8 reclassification data
NEWS	12	JAN 22	CA/CAPlus updated with revised CAS roles
NEWS	13	JAN 22	CA/CAPlus enhanced with patent applications from India
NEWS	14	JAN 29	PHAR reloaded with new search and display fields
NEWS	15	JAN 29	CAS Registry Number crossover limit increased to 300,000 in
			multiple databases
NEWS	16	FEB 15	PATDPASPC enhanced with Drug Approval numbers
NEWS	17	FEB 15	RUSSIAPAT enhanced with pre-1994 records
NEWS	18	FEB 23	KOREAPAT enhanced with IPC 8 features and functionality
NEWS	19	FEB 26	MEDLINE reloaded with enhancements
NEWS	20	FEB 26	EMBASE enhanced with Clinical Trial Number field
NEWS	21	FEB 26	TOXCENTER enhanced with reloaded MEDLINE
NEWS	22	FEB 26	IFICDB/IFIPAT/IFIUDB reloaded with enhancements
NEWS	23	FEB 26	CAS Registry Number crossover limit increased from 10,000

to 300,000 in multiple databases

NEWS 24 MAR 15 WPIDS/WPIX enhanced with new FRAGHITSTR display
format

NEWS 25 MAR 16 CASREACT coverage extended

NEWS 26 MAR 20 MARPAT now updated daily

NEWS 27 MAR 22 LWPI reloaded

NEWS 28 MAR 30 RDISCLOSURE reloaded with enhancements

NEWS 29 MAR 30 INPADOCDB will replace INPADOC on STN

NEWS 30 APR 02 JICST-EPLUS removed from database clusters and STN

NEWS EXPRESS NOVEMBER 10 CURRENT WINDOWS VERSION IS V8.01c, CURRENT
MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
AND CURRENT DISCOVER FILE IS DATED 25 SEPTEMBER 2006.

NEWS HOURS STN Operating Hours Plus Help Desk Availability

NEWS LOGIN Welcome Banner and News Items

NEWS IPC8 For general information regarding STN implementation
of IPC 8

NEWS X25 X.25 communication option no longer available

Enter NEWS followed by the item number or name to see news on that
specific topic.

All use of STN is subject to the provisions of the STN Customer
agreement. Please note that this agreement limits use to scientific
research. Use for software development or design or implementation
of commercial gateways or other similar uses is prohibited and may
result in loss of user privileges and other penalties.

* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 10:55:08 ON 05 APR 2007

=> File Medline EMBASE Biosis Caplus
COST IN U.S. DOLLARS

	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'MEDLINE' ENTERED AT 10:55:18 ON 05 APR 2007

FILE 'EMBASE' ENTERED AT 10:55:18 ON 05 APR 2007
Copyright (c) 2007 Elsevier B.V. All rights reserved.

FILE 'BIOSIS' ENTERED AT 10:55:18 ON 05 APR 2007
Copyright (c) 2007 The Thomson Corporation

FILE 'CAPLUS' ENTERED AT 10:55:18 ON 05 APR 2007
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2007 AMERICAN CHEMICAL SOCIETY (ACS)

=> s (chymotrypsin or trypsin or elastase or cathepsin or granzyme or chymase or tryptase) (4A) (domain or fragment or subunit or region or epitope or motif)

L1 6054 (CHYMOTRYPSIN OR TRYPSIN OR ELASTASE OR CATHEPSIN OR GRANZYME

OR CHYMASE OR TRYPTASE) (4A) (DOMAIN OR FRAGMENT OR SUBUNIT OR REGION OR EPITOPE OR MOTIF)

=> s (two hybrid)

L2 39797 (TWO HYBRID)

=> s l1 and l2

L3 11 L1 AND L2

=> duplicate

ENTER REMOVE, IDENTIFY, ONLY, OR (?):remove

ENTER L# LIST OR (END):l3

DUPLICATE PREFERENCE IS 'MEDLINE, EMBASE, BIOSIS, CAPLUS'

KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n

PROCESSING COMPLETED FOR L3

L4 5 DUPLICATE REMOVE L3 (6 DUPLICATES REMOVED)

=> d l4 1-5 bib ab

L4 ANSWER 1 OF 5 CAPLUS COPYRIGHT 2007 ACS on STN

AN 2004:218251 CAPLUS

DN 140:370674

TI The SANT2 Domain of the Murine Tumor Cell DnaJ-like Protein 1 Human

Homologue Interacts with α 1-Antichymotrypsin and Kinetically Interferes with Its Serpin Inhibitory Activity

AU Kroczyńska, Barbara; Evangelista, Christina M.; Samant, Shalaka S.;

Elguindi, Ebrahim C.; Blond, Sylvie Y.

CS Department of Medicinal Chemistry and Pharmacognosy, College of Pharmacy,

Center for Pharmaceutical Biotechnology, University of Illinois, Chicago,

IL, 60607-7173, USA

SO Journal of Biological Chemistry (2004), 279(12), 11432-11443. CODEN: JBCHA3; ISSN: 0021-9258

PB American Society for Biochemistry and Molecular Biology

DT Journal

LA English

AB The murine tumor cell DnaJ-like protein 1 or MTJ1/ERdj1 is a membrane

J-domain protein enriched in microsomal and nuclear fractions.

We

previously showed that its luminal J-domain stimulates the ATPase activity

of the mol. chaperone BiP/GRP78 (Chevalier, M., Rhee, H., Elguindi, E. C., and Blond, S. Y. (2000) J. Biol. Chemical 275, 19620-19627). MTJ1/ERdj1 also

contains a large carboxyl-terminal cytosolic extension composed of two

tryptophan-mediated repeats or SANT domains for which the function(s) is

unknown. Here we describe the cloning of the human homolog HTJ1 and its

interaction with α 1-antichymotrypsin (ACT), a member of the serine

proteinase inhibitor (serpin) family. The interaction was initially

identified in a two-hybrid screening and further confirmed in vitro by dot blots, native electrophoresis, and fluorescence

studies. The second SANT domain of HTJ1 (SANT2) was found to be sufficient for binding to ACT, both in yeast and in vitro.

Single

tryptophan-alanine substitutions at two strictly conserved residues

significantly (Trp-497) or totally (Trp-520) abolished the interaction

with ACT. SANT2 binds to human ACT with an intrinsic affinity equal to

0.5 nM. Preincubation of ACT with nearly stoichiometric concns. of SANT2

wild-type but not SANT2:W520A results in an apparent loss of ACT inhibitory activity toward chymotrypsin. Kinetic anal.

indicates that the

formation of the covalent inhibitory complex ACT-chymotrypsin is significantly delayed in the presence of SANT2 with no change on the

catalytic efficiency of the enzyme. This work demonstrates for the first

time that the SANT2 domain of MTJ1/HTJ1/ERdj1 mediates stable and high

affinity protein-protein interactions.

RE.CNT 72 THERE ARE 72 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2007 ACS on STN

AN 2003:656314 CAPLUS

DN 139:194002

TI Combinatorial libraries of protein monomer domains and their use
in

developing proteins with novel binding and interaction properties

IN Kolkman, Joost A.; Stemmer, Willem P. C.; Govindarajan, Sridhar

PA USA

SO U.S. Pat. Appl. Publ., 118 pp., Cont.-in-part of U.S. Ser. No.

133,128.

CODEN: USXXCO

DT Patent
LA English
FAN.CNT 11

PATENT NO.	KIND	DATE	APPLICATION NO.
DATE			
-----	----	-----	-----
PI US 2003157561	A1	20030821	US 2002-289660
20021106			
WO 2002088171	A2	20021107	WO 2002-US13257
20020426			
WO 2002088171	A3	20030508	
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA,			
CH, CN,			
CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD,			
GE, GH,			
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,			
LK, LR,			
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ,			
OM, PH,			
PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR,			
TT, TZ,			
UA, UG, UZ, VN, YU, ZA, ZM, ZW			
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM,			
AZ, BY,			
KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI,			
FR, GB,			
GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI,			
CM, GA,			
GN, GQ, GW, ML, MR, NE, SN, TD, TG			
US 2003082630	A1	20030501	US 2002-133128
20020426			
US 2004175756	A1	20040909	US 2003-693057
20031024			
US 2005048512	A1	20050303	US 2003-693056
20031024			
CA 2504670	A1	20040527	CA 2003-2504670
20031106			
WO 2004044011	A2	20040527	WO 2003-US35664
20031106			
WO 2004044011	A3	20060420	
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA,			
CH, CN,			
CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB,			
GD, GE,			
GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ,			
LC, LK,			
LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI,			
NO, NZ,			
OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY,			
TJ, TM,			

TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
 RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW,
 AM, AZ,
 BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE,
 DK, EE,
 ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE,
 SI, SK,
 TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE,
 SN, TD, TG

AU 2003295426 A1 20040603 AU 2003-295426

20031106

EP 1587843 A2 20051026 EP 2003-786612

20031106

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE,
 MC, PT,

IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU,
 SK

US 2005053973 A1 20050310 US 2004-840723

20040505

US 2005089932 A1 20050428 US 2004-871602

20040617

US 2006223114 A1 20061005 US 2005-281245

20051116

US 2006286603 A1 20061221 US 2006-392108

20060328

PRAI US 2001-337209P P 20011119

US 2001-333359P P 20011126

US 2002-374107P P 20020418

US 2002-133128 A2 20020426

WO 2002-US13257 A 20020426

US 2001-286823P P 20010426

US 2002-289660 A2 20021106

US 2003-693056 A2 20031024

US 2003-693057 A2 20031024

WO 2003-US35664 W 20031106

US 2004-840723 A2 20040505

US 2004-871602 A2 20040617

US 2004-628596P P 20041116

OS MARPAT 139:194002

AB Combinatorial libraries of variants of discrete and defined monomer

domains of proteins and immunodomains are described for use in protein

engineering. Methods for generating multimers from two or more selected

discrete monomer domains are also provided, along with methods for

identifying multimers possessing a desired property.

Presentation systems

are also provided which present the discrete monomer and/or

immuno-domains, selected monomer and/or immuno-domains,

multimers and/or

selected multimers to allow their selection. Compns., libraries and cells that express one or more library member, along with kits and integrated systems, are also included in the present invention.

L4 ANSWER 3 OF 5 MEDLINE on STN DUPLICATE 1
AN 2000437199 MEDLINE
DN PubMed ID: 10821830
TI Self-assembly and supramolecular organization of EMILIN.
AU Mongiat M; Mungiguerra G; Bot S; Mucignat M T; Giacomello E; Doliana R; Colombatti A
CS Divisione di Oncologia Sperimentale 2, Centro di Riferimento Oncologico di Aviano, Italy.
SO The Journal of biological chemistry, (2000 Aug 18) Vol. 275, No. 33, pp. 25471-80.
Journal code: 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 200009
ED Entered STN: 28 Sep 2000
Last Updated on STN: 28 Sep 2000
Entered Medline: 21 Sep 2000
AB The primary structure of human Elastin microfibril interface-located protein (EMILIN), an elastic fiber-associated glycoprotein, consists of a globular Clq domain (gClq) at the C terminus, a short collagenous stalk, a long region with a high potential for forming coiled-coil alpha helices, and a cysteine-rich N-terminal sequence. It is not known whether the EMILIN gClq domain is involved in the assembly process and in the supramolecular organization as shown for the similar domain of collagen X.
By employing the yeast two-hybrid system the EMILIN gClq domains interacted with themselves, proving for the first time that this interaction occurs in vivo. The gClq domain formed oligomers running as trimers in native gels that were less stable than the comparable trimers of the collagen X gClq domain since they did not withstand

heating. The collagenous domain was trypsin-resistant and migrated at a size corresponding to a triple helix under native conditions. In reducing agarose gels, EMILIN also migrated as a trimer, whereas under non-reducing conditions it formed polymers of many millions of daltons. A truncated fragment lacking gClq and collagenous domains assembled to a much lesser extent, thus deducing that the C-terminal domain(s) are essential for the formation of trimers that finally assemble into large EMILIN multimers.

L4 ANSWER 4 OF 5 MEDLINE on STN DUPLICATE 2

AN 1999429835 MEDLINE

DN PubMed ID: 10498700

TI P1 ParB domain structure includes two independent multimerization domains.

AU Surtees J A; Funnell B E

CS Department of Molecular and Medical Genetics, University of Toronto,

Toronto, Ontario M5S 1A8, Canada.

SO Journal of bacteriology, (1999 Oct) Vol. 181, No. 19, pp. 5898-908.

Journal code: 2985120R. ISSN: 0021-9193.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)

LA English

FS Priority Journals

EM 199910

ED Entered STN: 1 Nov 1999

Last Updated on STN: 3 Mar 2000

Entered Medline: 21 Oct 1999

AB ParB is one of two P1-encoded proteins that are required for active

partition of the P1 prophage in Escherichia coli. To probe the native

domain structure of ParB, we performed limited proteolytic digestions of

full-length ParB, as well as of several N-terminal and C-terminal deletion

fragments of ParB. The C-terminal 140 amino acids of ParB form a very

trypsin-resistant domain. In contrast, the N terminus

is more susceptible to proteolysis, suggesting that it forms a less stably

folded domain or domains. Because native ParB is a dimer in solution, we

analyzed the ability of ParB fragments to dimerize, using both the yeast two-hybrid system and in vitro chemical cross-linking of purified proteins. These studies revealed that the C-terminal 59 amino acids of ParB, a region within the protease-resistant domain, are sufficient for dimerization. Cross-linking and yeast two-hybrid experiments also revealed the presence of a second self-association domain within the N-terminal half of ParB. The cross-linking data also suggest that the C terminus is inhibitory to multimerization through the N-terminal domain in vitro. We propose that the two multimerization domains play distinct roles in partition complex formation.

L4 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2007 ACS on STN

AN 1998:801698 CAPLUS

DN 130:135848

TI The β subunit of CKII interacts with the lysosomal protease cathepsin

L

AU Yu, Hyun Jae; Ahn, Bong-Hyun; Bae, Young-Seuk

CS Department of Biochemistry, College of Natural Sciences, Kyungpook

National University, Taegu, 702-701, S. Korea

SO Journal of Biochemistry and Molecular Biology (1998), 31(6), 611-614

CODEN: JBMBE5; ISSN: 1225-8687

PB Springer-Verlag Singapore Pte. Ltd.

DT Journal

LA English

AB Protein kinase CKII is a protein Ser/Thr kinase that is ubiquitously

distributed in eukaryotic cells. Although it has been suggested that CKII

plays an critical role in cell growth and proliferation, its functional

significance and regulation in the cells remain poorly understood. To

investigate the exact biol. function of CKII, the authors have identified

proteins that interact with the subunits of CKII using the two-hybrid system. The authors have identified cathepsin L, a lysosomal protease, as a cellular protein capable of interacting with the

β subunit of CKII. Cathepsin L does not interact with the α subunit of CKII, supporting the idea that the β subunit can mediate

the interaction of CKII with target proteins. The authors have found that

cathepsin L has several putative CKII phosphorylation sites including Thr

84, Ser 160, Ser 270, Thr 288, and Ser 301. These data suggest that CKII

is a possible protein kinase for cathepsin L phosphorylation.

RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> s (reconstitution or complementation) (4A) activity

L5 4422 (RECONSTITUTION OR COMPLEMENTATION) (4A) ACTIVITY

=> s l1 and l5

L6 5 L1 AND L5

=> duplicate

ENTER REMOVE, IDENTIFY, ONLY, OR (?):remove

ENTER L# LIST OR (END):16

DUPLICATE PREFERENCE IS 'MEDLINE, EMBASE, BIOSIS, CAPLUS'

KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n

PROCESSING COMPLETED FOR L6

L7 3 DUPLICATE REMOVE L6 (2 DUPLICATES REMOVED)

=> d l7 1-3 bib ab

L7 ANSWER 1 OF 3 MEDLINE on STN DUPLICATE 1
AN 93350342 MEDLINE
DN PubMed ID: 8347934
TI Activation and secretion of Serratia hemolysin.
AU Braun V; Ondraczek R; Hobbie S
CS Mikrobiologie II, Universitat Tübingen, Germany.
SO Zentralblatt für Bakteriologie : international journal of medical
microbiology, (1993 Apr) Vol. 278, No. 2-3, pp. 306-15. Ref: 28
Journal code: 9203851. ISSN: 0934-8840.
CY GERMANY: Germany, Federal Republic of
DT (IN VITRO)
Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
General Review; (REVIEW)
LA English
FS Priority Journals
EM 199309
ED Entered STN: 1 Oct 1993
Last Updated on STN: 3 Mar 2000
Entered Medline: 16 Sep 1993
AB The hemolysin of Serratia marcescens (Sh1A) is secreted into the
culture
medium and forms small pores of a defined size in erythrocytes
and in
black lipid membranes. The protein is synthesized as an inactive
precursor of 1608 residues which is translocated across the
cytoplasmic

membrane by the Sec-export system. In the absence of the outer membrane protein ShlB, the ShlA protein (designated ShlA*) stays in the periplasm and displays about 0.1% of the activity of the secreted form. Secretion of ShlA with the help of ShlB is accompanied by its conversion to the hemolytic form. A ShlA derivative consisting of the N-terminal 238 residues of ShlA is secreted by ShlB, showing that the secretion signal resides in the amino terminal part of ShlA. ShlA* can be activated in vitro by a cell lysate containing ShlB, the activated ShlA remains hemolytic upon removal of ShlB. The assumed covalent modification of ShlA* by ShlB occurs in the N-terminus of ShlA since an amino terminal fragment (M(r) 28,000) secreted by ShlB, and a trypsin fragment of ShlA (M(r) 15,000) are both able to convert ShlA* to a hemolytic protein. In contrast to the permanent modification of ShlA* by ShlB, ShlA activity achieved by complementation with the ShlA fragments is abolished upon removal of the fragments. Apparently, the N-terminal portion of ShlA contains the information for secretion through the outer membrane and for insertion into the erythrocyte membrane. This information is lacking in ShlA* formed in the absence of ShlB but contained in the ShlA fragments formed in the presence of ShlB. The latter bind to ShlA* and direct ShlA* into the erythrocyte membrane. The fragments themselves are too short to build pores. The HpmA hemolysin of *Proteus mirabilis* shows extensive homology to ShlA. In vitro activation of HpmA* by ShlB and complementation by the 28 kDa ShlA fragment indicates a common activation mechanism.

L7 ANSWER 2 OF 3 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights

reserved on STN

DUPLICATE 2

AN 78366209 EMBASE

DN 1978366209

TI Some effects of trypsin on the subunits of the membrane ATPase from

Escherichia coli.

AU Smith J.B.; Sternweis P.C.; Larson R.J.

CS Sect. Biochem., Molec. Cell Biol., Cornell Univ., Ithaca, N.Y.
14853,

United States

SO Progress in Clinical and Biological Research, (1978) Vol.
VOL.22, pp.

545-552.

CODEN: PCBRD2

CY United States

DT Journal

FS 004 Microbiology
029 Clinical Biochemistry

LA English

AB Five-subunit (α , β , γ , δ , ϵ) F1-ATPase from
E. coli (ECF1) was reconstituted by combining 2 mixtures of
inactive

subunits (an $\alpha\beta$ fraction and a $\gamma\epsilon$ -rich one) and
the purified δ subunit. The combination of $\alpha\beta$ and
 $\gamma\epsilon$ -rich fractions was sufficient for reconstituting ATPase
activity, which was achieved by dialyzing the subunits at 23° C

in
the presence of Mg-ATP. Addition of the purified δ subunit to
the

reconstituted ATPase restored coupling factor activity to the
enzyme. The

reconstituted enzyme was as active as the native enzyme in
restoring

ATP-driven transhydrogenase activity to F1-depleted vesicles.
Incubation

of the $\gamma\epsilon$ -rich fraction with trypsin decreased markedly the
reconstitution of ATPase activity, whereas treatment of
the $\alpha\beta$ fraction with trypsin under the same conditions had no
significant effect. ECF1 containing only the α and β subunits,
which was prepared by trypsin digestion, was highly active

hydrolytically

but remained inactive as a coupling factor even after the
addition of the

$\gamma\epsilon$ -rich fraction and δ . The inhibition of ECF1 by the
purified ϵ subunit was reversed by trypsin.

Thus, while trypsin inactivates the γ and ϵ subunits of
ECF1, the α and/or β subunits are altered in a way which only
inactivates the coupling factor activity of the enzyme without
affecting

its ATPase activity or the reconstitution of ATPase
activity after cold inactivation. Since exposure of the α
and β subunits to trypsin does not appear to alter their

interaction

with added γ and ϵ , it may be that the loss of coupling
factor activity is due to a modification in α or β which
disrupts their interaction with the membrane attachment subunit

(8).

L7 ANSWER 3 OF 3 BIOSIS COPYRIGHT (c) 2007 The Thomson
Corporation on STN
AN 1979:141571 BIOSIS
DN PREV197967021571; BA67:21571
TI THE FOLDING OF PANCREATIC ELASTASE INDEPENDENT DOMAIN
RE FOLDING AND INTER DOMAIN INTERACTION.
AU GHELIS C [Reprint author]; TEMPETE-GAILLOURDET M; YON J M
CS LAB ENZYMOL PHYS-CHIM MOL, UNIV PARIS-SUD, 91405, ORSAY, FR
SO Biochemical and Biophysical Research Communications, (1978) Vol.
84, No.
1, pp. 31-36.
CODEN: BBRCA9. ISSN: 0006-291X.
DT Article
FS BA
LA ENGLISH
AB The role of domains in the refolding of [pig pancreatic] elastase
, a 2 domain protein, was investigated. Fragment 126-245,
corresponding to 1 of the 2 domains, is able to refold
independently. The
in vitro complementation of the 2 domains lead to a molecule
having the
overall conformation of the native protein and only a weak but
significant
activity.

=> s 14 and 17

L8 0 L4 AND L7

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:SSPTASXS1656

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * Welcome to STN International * * * * *
* *

NEWS	1		Web Page URLs for STN Seminar Schedule - N. America
NEWS	2		"Ask CAS" for self-help around the clock
NEWS	3	DEC 18	CA/CAPLUS pre-1967 chemical substance index entries enhanced
			with preparation role
NEWS	4	DEC 18	CA/CAPLUS patent kind codes updated
NEWS	5	DEC 18	MARPAT to CA/CAPLUS accession number crossover limit increased
			to 50,000
NEWS	6	DEC 18	MEDLINE updated in preparation for 2007 reload
NEWS	7	DEC 27	CA/CAPLUS enhanced with more pre-1907 records
NEWS	8	JAN 08	CHEMLIST enhanced with New Zealand Inventory of Chemicals
NEWS	9	JAN 16	CA/CAPLUS Company Name Thesaurus enhanced and reloaded
NEWS	10	JAN 16	IPC version 2007.01 thesaurus available on STN
NEWS	11	JAN 16	WPIDS/WPINDEX/WPIX enhanced with IPC 8 reclassification data
NEWS	12	JAN 22	CA/CAPLUS updated with revised CAS roles
NEWS	13	JAN 22	CA/CAPLUS enhanced with patent applications from India
NEWS	14	JAN 29	PHAR reloaded with new search and display fields
NEWS	15	JAN 29	CAS Registry Number crossover limit increased to 300,000 in
			multiple databases
NEWS	16	FEB 15	PATDPASPC enhanced with Drug Approval numbers
NEWS	17	FEB 15	RUSSIAPAT enhanced with pre-1994 records
NEWS	18	FEB 23	KOREAPAT enhanced with IPC 8 features and functionality
NEWS	19	FEB 26	MEDLINE reloaded with enhancements
NEWS	20	FEB 26	EMBASE enhanced with Clinical Trial Number field
NEWS	21	FEB 26	TOXCENTER enhanced with reloaded MEDLINE
NEWS	22	FEB 26	IFICDB/IFIPAT/IFIUDB reloaded with enhancements
NEWS	23	FEB 26	CAS Registry Number crossover limit increased from 10,000

to 300,000 in multiple databases

NEWS 24 MAR 15 WPIDS/WPIX enhanced with new FRAGHITSTR display
format

NEWS 25 MAR 16 CASREACT coverage extended

NEWS 26 MAR 20 MARPAT now updated daily

NEWS 27 MAR 22 LWPI reloaded

NEWS 28 MAR 30 RDISCLOSURE reloaded with enhancements

NEWS 29 MAR 30 INPADOCDB will replace INPADOC on STN

NEWS 30 APR 02 JICST-EPLUS removed from database clusters and STN

NEWS EXPRESS NOVEMBER 10 CURRENT WINDOWS VERSION IS V8.01c, CURRENT
MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
AND CURRENT DISCOVER FILE IS DATED 25 SEPTEMBER 2006.

NEWS HOURS STN Operating Hours Plus Help Desk Availability

NEWS LOGIN Welcome Banner and News Items

NEWS IPC8 For general information regarding STN implementation
of IPC 8

NEWS X25 X.25 communication option no longer available

Enter NEWS followed by the item number or name to see news on that
specific topic.

All use of STN is subject to the provisions of the STN Customer
agreement. Please note that this agreement limits use to scientific
research. Use for software development or design or implementation
of commercial gateways or other similar uses is prohibited and may
result in loss of user privileges and other penalties.

* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 09:56:15 ON 05 APR 2007

=> File Medline EMBASE Biosis Caplus

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'MEDLINE' ENTERED AT 09:56:27 ON 05 APR 2007

FILE 'EMBASE' ENTERED AT 09:56:27 ON 05 APR 2007

Copyright (c) 2007 Elsevier B.V. All rights reserved.

FILE 'BIOSIS' ENTERED AT 09:56:27 ON 05 APR 2007

Copyright (c) 2007 The Thomson Corporation

FILE 'CAPLUS' ENTERED AT 09:56:27 ON 05 APR 2007

USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.

PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

COPYRIGHT (C) 2007 AMERICAN CHEMICAL SOCIETY (ACS)

=> s (protease or peptidase or proteinase) (4A) (domain or fragment
or subunit or region eptitope or motif)
L1 11554 (PROTEASE OR PEPTIDASE OR PROTEINASE) (4A) (DOMAIN OR
FRAGMENT

OR SUBUNIT OR REGION EPTITOPe OR MOTIF)

=> s reconstitution (4A) activity
L2 3341 RECONSTITUTION (4A) ACTIVITY

=> s l1 (10A) l2
L3 0 L1 (10A) L2

=> s l1 and l2
L4 3 L1 AND L2

=> duplicate
ENTER REMOVE, IDENTIFY, ONLY, OR (?):remove
ENTER L# LIST OR (END):l4
DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS, CAPLUS'
KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n
PROCESSING COMPLETED FOR L4
L5 1 DUPLICATE REMOVE L4 (2 DUPLICATES REMOVED)

=> d l5 1 bib ab

L5 ANSWER 1 OF 1 MEDLINE on STN DUPLICATE 1
AN 89214013 MEDLINE
DN PubMed ID: 2854124
TI Carboxyl-terminal truncation and site-directed mutagenesis of
the EF hand
structure-domain of the small subunit of rabbit
calcium-dependent protease.
AU Minami Y; Emori Y; Imajoh-Ohmi S; Kawasaki H; Suzuki K
CS Department of Molecular Biology, Tokyo Metropolitan Institute of
Medical
Science.
SO Journal of biochemistry, (1988 Dec) Vol. 104, No. 6, pp. 927-33.
Journal code: 0376600. ISSN: 0021-924X.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 198905
ED Entered STN: 6 Mar 1990
Last Updated on STN: 6 Mar 1990
Entered Medline: 26 May 1989
AB A mutant of the small subunit of rabbit calcium-dependent
protease lacking the amino-terminal one-fourth produced in

Escherichia coli could associate with the native large subunit to exert protease activity. Deletion of a few carboxyl-terminal residues of this variant small subunit caused a significant decrease in the protease activity after reconstitution with the native large subunit. Loss of the fourth EF hand loop region by further truncation of the variant small subunit made interaction with the large subunit impossible. The calcium binding assay revealed that the fourth EF hand structure of the rabbit small subunit, which has been previously demonstrated to possess two calcium-binding sites, can bind calcium ions. Furthermore it was established by site-directed mutagenesis that the first EF hand structure, in addition to the fourth one, is capable of binding calcium ions. Replacement of amino acids in the EF hand structure affected interaction with the native large subunit or the calcium sensitivity of the reconstituted product. These findings indicate that the EF hand structure-domain of the small subunit is essential for the full protease activity.

=> s complementation (4A) activity
L6 1091 COMPLEMENTATION (4A) ACTIVITY

=> s l1 (10A) l6
L7 0 L1 (10A) L6

=> s l1 and l6
L8 8 L1 AND L6

=> duplicate
ENTER REMOVE, IDENTIFY, ONLY, OR (?):remove
ENTER L# LIST OR (END):l8
DUPLICATE PREFERENCE IS 'MEDLINE, EMBASE, BIOSIS, CAPLUS'
KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n
PROCESSING COMPLETED FOR L8
L9 3 DUPLICATE REMOVE L8 (5 DUPLICATES REMOVED)

=> d l9 1-3 bib ab

L9 ANSWER 1 OF 3 MEDLINE on STN DUPLICATE 1
AN 2007002178 MEDLINE
DN PubMed ID: 17101804
TI Variable and tissue-specific subunit composition of
mitochondrial m-AAA
protease complexes linked to hereditary spastic paraplegia.
AU Koppen Mirko; Metodiev Metodi D; Casari Giorgio; Rugarli Elena
I; Langer
Thomas
CS Institut fur Genetik, Universitat zu Koln, Zulpicher Strasse,
0674 Koln,
Germany.
SO Molecular and cellular biology, (2007 Jan) Vol. 27, No. 2, pp.
758-67.
Electronic Publication: 2006-11-13.
Journal code: 8109087. ISSN: 0270-7306.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 200702
ED Entered STN: 4 Jan 2007
Last Updated on STN: 6 Feb 2007
Entered Medline: 5 Feb 2007
AB The m-AAA protease, an ATP-dependent proteolytic complex in the
mitochondrial inner membrane, controls protein quality and
regulates
ribosome assembly, thus exerting essential housekeeping
functions within
mitochondria. Mutations in the m-AAA protease subunit

paraplegin cause axonal degeneration in hereditary spastic paraplegia (HSP), but the basis for the unexpected tissue specificity is not understood. Paraplegin assembles with homologous Afg3l2 subunits into hetero-oligomeric complexes which can substitute for yeast m-AAA proteases, demonstrating functional conservation. The function of a third paralogue, Afg3l1 expressed in mouse, is unknown. Here, we analyze the assembly of paraplegin into m-AAA complexes and monitor consequences of paraplegin deficiency in HSP fibroblasts and in a mouse model for HSP. Our findings reveal variability in the assembly of m-AAA proteases in mitochondria in different tissues. Homo-oligomeric Afg3l1 and Afg3l2 complexes and hetero-oligomeric assemblies of both proteins with paraplegin can be formed. Yeast complementation studies demonstrate the proteolytic activity of these assemblies. Paraplegin deficiency in HSP does not result in the loss of m-AAA protease activity in brain mitochondria. Rather, homo-oligomeric Afg3l2 complexes accumulate, and these complexes can substitute for housekeeping functions of paraplegin-containing m-AAA complexes. We therefore propose that the formation of m-AAA proteases with altered substrate specificities leads to axonal degeneration in HSP.

L9 ANSWER 2 OF 3 MEDLINE on STN DUPLICATE 2
 AN 1999126015 MEDLINE
 DN PubMed ID: 9928935
 TI The protease activity of a calpain-like cysteine protease in *Saccharomyces cerevisiae* is required for alkaline adaptation and sporulation.
 AU Futai E; Maeda T; Sorimachi H; Kitamoto K; Ishiura S; Suzuki K
 CS Department of Molecular Biology, Institute of Molecular and Cellular Biosciences, University of Tokyo, Japan.
 SO Molecular & general genetics : MGG, (1999 Jan) Vol. 260, No. 6, pp. 559-68.
 Journal code: 0125036. ISSN: 0026-8925.
 CY GERMANY: Germany, Federal Republic of
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals

EM 199902
ED Entered STN: 1 Mar 1999
Last Updated on STN: 3 Mar 2000
Entered Medline: 18 Feb 1999
AB Abstract *Saccharomyces cerevisiae* has only one putative gene (designated CPL1) for a cysteine protease with a protease domain similar to that of calpain. This gene product shows significant sequence similarity to PalBp, a fungal (*Emmericella nidulans*) calpain-like protease that is responsible for adaptation under alkaline conditions, both in the protease domain and the domain following the protease domain. CPL1 disruptant strains show impaired growth at alkaline pH, but no obvious growth defects under acidic pH conditions. This phenotype is complemented by the wild-type CPL1 gene, and its protease activity is essential for complementation. Disruption of CPL1 also causes reduced sporulation efficiency and promotes the degradation of the transcription factor Rim101p, which is involved in the sporulation pathway and has been shown to accumulate in a C-terminally truncated, active form under alkaline conditions. Furthermore, expression of the C-terminally truncated Rim101p suppressed the alkaline sensitivity associated with CPL1 disruption. These results indicate that a calpain-like cysteine protease, Cpl1p, plays an important role in alkaline adaptation and sporulation processes, via regulation of the turnover and processing of the transcription factor Rim101p.

L9 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1999:112529 CAPLUS
DN 130:308897
TI The protease activity of a calpain-like cysteine protease in *Saccharomyces cerevisiae* is required for alkaline adaptation and sporulation
AU Futai, E.; Maeda, T.; Sorimachi, H.; Kitamoto, K.; Ishiura, S.; Suzuki, K.
CS Laboratory of Molecular Structure and Function Department of Molecular Biology Institute of Molecular and Cellular Biosciences, University of Tokyo, Tokyo, 113-0032, Japan
SO Molecular and General Genetics (1998), 260(6), 559-568

CODEN: MGGEAE; ISSN: 0026-8925

PB Springer-Verlag

DT Journal

LA English

AB *Saccharomyces cerevisiae* has only one putative gene (designated CPL1) for

a cysteine protease with a protease domain similar to that of calpain. This gene product shows significant sequence

similarity to PalBp, a fungal (*Emmericella nidulans*) calpain-like protease

that is responsible for adaptation under alkaline conditions, both in the

protease domain and the domain following the protease domain. CPL1 disruptant strains show impaired growth at alkaline pH, but no obvious growth defects under acidic pH

conditions. This phenotype is complemented by the wild-type CPL1 gene,

and its protease activity is essential for complementation. Disruption of CPL1 also causes reduced sporulation efficiency and promotes the degradation of the transcription

factor Rim101p, which is involved in the sporulation pathway and has been

shown to accumulate in a C-terminally truncated, active form under alkaline

conditions. Furthermore, expression of the C-terminally truncated Rim101p

suppressed the alkaline sensitivity associated with CPL1 disruption. These

results indicate that a calpain-like cysteine protease, Cpl1p, plays an

important role in alkaline adaptation and sporulation processes, via

regulation of the turnover and processing of the transcription factor

Rim101p.

RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=>

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L3	2651401	s (chymotrypsin or trypsin or elastase or cathepsin or granzyme or chymase or tryptase) near4 (domain or fragment or subunit or region or epitope or motif)	US-PGPUB; USPAT	OR	OFF	2007/04/05 11:23
L4	2523	(chymotrypsin or trypsin or elastase or cathepsin or granzyme or chymase or tryptase) near4 (domain or fragment or subunit or region or epitope or motif)	US-PGPUB; USPAT	OR	OFF	2007/04/05 11:26
L5	3426	(reconstitution or complementation) near4 activity	US-PGPUB; USPAT	OR	OFF	2007/04/05 11:24
L6	0	I4 near10 I5	US-PGPUB; USPAT	OR	OFF	2007/04/05 11:24
L7	123	I4 and I5	US-PGPUB; USPAT	OR	OFF	2007/04/05 11:24
L8	0	I4 same 5	US-PGPUB; USPAT	OR	OFF	2007/04/05 11:25
L9	0	I4 near30 I5	US-PGPUB; USPAT	OR	OFF	2007/04/05 11:25
L10	117	I7 and (two adj hybrid)	US-PGPUB; USPAT	OR	OFF	2007/04/05 11:25
L11	153	(chymotrypsin or trypsin or elastase or cathepsin or granzyme or chymase or tryptase) near4 (fusion adj protein)	US-PGPUB; USPAT	OR	OFF	2007/04/05 11:26
L12	0	I10 and I11	US-PGPUB; USPAT	OR	OFF	2007/04/05 11:26

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:SSPTASXS1656

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * Welcome to STN International * * * * *
* *

NEWS	1		Web Page URLs for STN Seminar Schedule - N. America
NEWS	2		"Ask CAS" for self-help around the clock
NEWS	3	DEC 18	CA/CAPplus pre-1967 chemical substance index entries enhanced
			with preparation role
NEWS	4	DEC 18	CA/CAPplus patent kind codes updated
NEWS	5	DEC 18	MARPAT to CA/CAPplus accession number crossover limit increased
			to 50,000
NEWS	6	DEC 18	MEDLINE updated in preparation for 2007 reload
NEWS	7	DEC 27	CA/CAPplus enhanced with more pre-1907 records
NEWS	8	JAN 08	CHEMLIST enhanced with New Zealand Inventory of Chemicals
NEWS	9	JAN 16	CA/CAPplus Company Name Thesaurus enhanced and reloaded
NEWS	10	JAN 16	IPC version 2007.01 thesaurus available on STN
NEWS	11	JAN 16	WPIDS/WPINDEX/WPIX enhanced with IPC 8 reclassification data
NEWS	12	JAN 22	CA/CAPplus updated with revised CAS roles
NEWS	13	JAN 22	CA/CAPplus enhanced with patent applications from India
NEWS	14	JAN 29	PHAR reloaded with new search and display fields
NEWS	15	JAN 29	CAS Registry Number crossover limit increased to 300,000 in
			multiple databases
NEWS	16	FEB 15	PATDPASPC enhanced with Drug Approval numbers
NEWS	17	FEB 15	RUSSIAPAT enhanced with pre-1994 records
NEWS	18	FEB 23	KOREAPAT enhanced with IPC 8 features and functionality
NEWS	19	FEB 26	MEDLINE reloaded with enhancements
NEWS	20	FEB 26	EMBASE enhanced with Clinical Trial Number field
NEWS	21	FEB 26	TOXCENTER enhanced with reloaded MEDLINE
NEWS	22	FEB 26	IFICDB/IFIPAT/IFIUDB reloaded with enhancements
NEWS	23	FEB 26	CAS Registry Number crossover limit increased from 10,000

to 300,000 in multiple databases

NEWS 24 MAR 15 WPIDS/WPIX enhanced with new FRAGHITSTR display
format

NEWS 25 MAR 16 CASREACT coverage extended

NEWS 26 MAR 20 MARPAT now updated daily

NEWS 27 MAR 22 LWPI reloaded

NEWS 28 MAR 30 RDISCLOSURE reloaded with enhancements

NEWS 29 MAR 30 INPADOCDB will replace INPADOC on STN

NEWS 30 APR 02 JICST-EPLUS removed from database clusters and STN

NEWS EXPRESS NOVEMBER 10 CURRENT WINDOWS VERSION IS V8.01c, CURRENT
MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
AND CURRENT DISCOVER FILE IS DATED 25 SEPTEMBER 2006.

NEWS HOURS STN Operating Hours Plus Help Desk Availability

NEWS LOGIN Welcome Banner and News Items

NEWS IPC8 For general information regarding STN implementation
of IPC 8

NEWS X25 X.25 communication option no longer available

Enter NEWS followed by the item number or name to see news on that
specific topic.

All use of STN is subject to the provisions of the STN Customer
agreement. Please note that this agreement limits use to scientific
research. Use for software development or design or implementation
of commercial gateways or other similar uses is prohibited and may
result in loss of user privileges and other penalties.

* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 18:46:52 ON 12 APR 2007

=> File Medline EMBASE Biosis Caplus
COST IN U.S. DOLLARS

	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'MEDLINE' ENTERED AT 18:47:25 ON 12 APR 2007

FILE 'EMBASE' ENTERED AT 18:47:25 ON 12 APR 2007
Copyright (c) 2007 Elsevier B.V. All rights reserved.

FILE 'BIOSIS' ENTERED AT 18:47:25 ON 12 APR 2007
Copyright (c) 2007 The Thomson Corporation

FILE 'CAPLUS' ENTERED AT 18:47:25 ON 12 APR 2007
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2007 AMERICAN CHEMICAL SOCIETY (ACS)

=> S (picornavirus or potyvirus or rhinovirus or enterovirus or echovirus or (coxsackie virus) or (hepatitis virus) or cardiovirus) (4A) (cysteine protease)

L1 22 (PICORNAVIRUS OR POTYVIRUS OR RHINOVIRUS OR ENTEROVIRUS OR ECHOVIRUS OR (COXSACKIE VIRUS) OR (HEPATITIS VIRUS) OR CARDIOVIRUS) (4A) (CYSTEINE PROTEASE)

=> S L1 (8A) (reconstitution or (two-hybrid) or (2-hybrid) or complementation)

L2 0 L1 (8A) (RECONSTITUTION OR (TWO-HYBRID) OR (2-HYBRID) OR COMPLEMENTATION)

=> s l1 (8A) (domain or fragment)

L3 0 L1 (8A) (DOMAIN OR FRAGMENT)

=> s l1 (8A) structure

L4 0 L1 (8A) STRUCTURE

=> duplicate

ENTER REMOVE, IDENTIFY, ONLY, OR (?):remove

ENTER L# LIST OR (END):l1

DUPLICATE PREFERENCE IS 'MEDLINE, EMBASE, BIOSIS, CAPLUS'

KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n

PROCESSING COMPLETED FOR L1

L5 12 DUPLICATE REMOVE L1 (10 DUPLICATES REMOVED)

=> s (3C cysteine protease)

L6 16 (3C CYSTEINE PROTEASE)

=> S L6 (8A) (reconstitution or (two-hybrid) or (2-hybrid) or complementation)

L7 0 L6 (8A) (RECONSTITUTION OR (TWO-HYBRID) OR (2-HYBRID) OR COMPLEMENTATION)

=> s (trypsin or chymotrypsin) (8A) (reconstitution or (two-hybrid) or (2-hybrid) or complementation)

L8 117 (TRYPSIN OR CHYMOTRYPSIN) (8A) (RECONSTITUTION OR (TWO-HYBRID) OR (2-HYBRID) OR COMPLEMENTATION)

=> s (trypsin or chymotrypsin) (4A) (domain or fragment or fusion protein)

L9 3014 (TRYPSIN OR CHYMOTRYPSIN) (4A) (DOMAIN OR FRAGMENT OR FUSION PROTEIN)

=> s 18 and 19

L10 5 L8 AND L9

=> duplicate

ENTER REMOVE, IDENTIFY, ONLY, OR (?):remove

ENTER L# LIST OR (END):l10

DUPLICATE PREFERENCE IS 'MEDLINE, EMBASE, BIOSIS, CAPLUS'

KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):no

PROCESSING COMPLETED FOR L10

L11 2 DUPLICATE REMOVE L10 (3 DUPLICATES REMOVED)

=> d l11 1-2 bib ab

L11 ANSWER 1 OF 2 MEDLINE on STN DUPLICATE 1

AN 1998035059 MEDLINE

DN PubMed ID: 9367764

TI Complementation of peptide fragments of the single domain protein chymotrypsin inhibitor 2.

AU Ladurner A G; Itzhaki L S; de Prat Gay G; Fersht A R

CS MRC Cambridge Centre for Protein Engineering, MRC Centre, UK.

SO Journal of molecular biology, (1997 Oct 17) Vol. 273, No. 1, pp. 317-29.

Journal code: 2985088R. ISSN: 0022-2836.

CY ENGLAND: United Kingdom

DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)

LA English

FS Priority Journals

EM 199712

ED Entered STN: 9 Jan 1998

Last Updated on STN: 9 Jan 1998

Entered Medline: 5 Dec 1997

AB Chymotrypsin inhibitor 2 (CI2) folds kinetically as a single domain

protein. It has been shown that elements of native secondary structure do

not significantly form in fragments as the 64 residue protein is progressively increased in length from its N terminus, until at least 60

residues are present. Here, we analyse peptides of increasing length from

the C terminus and find that native-like structure is not present even in

the largest, fragment (7-64). We have examined sets of peptides of the

form (1 - x) and ((x + 1)-64) to detect complementation. The only pair

that readily complements and gives native-like structure is (1-40) and

(41-64), where cleavage occurs in the protease-binding loop of CI2. But,

all the pairs of peptides (1 - x) + (41-64) complement for x > 40, as do all pairs of (1-40) + (x-64), where x < 40. The resultant complexes appear to be equivalent to (1-40). (41-64) with the overlapping sequence being unstructured. Thus, the folding of CI2 is extremely co-operative, and interactions have to be made between subdomains (1-40) and (41-64). This is consistent with the mechanism proposed for the folding pathway of intact CI2 in which a diffuse nucleus is formed in the transition state between the alpha-helix in the N-terminal region of the protein and conserved hydrophobic contacts in the C-terminal region of the polypeptide. It is with these protein design features that CI2 can be an effective protease inhibitor.

L11 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2007 ACS on STN

AN 1994:429728 CAPLUS

DN 121:29728

TI Generation of a Family of Protein Fragments for Structure-Folding Studies.

1. Folding Complementation of Two Fragments of Chymotrypsin Inhibitor-2 Formed by Cleavage at Its Unique Methionine Residue

AU Prat Gay, G. de; Fersht, Alan R.

CS Department of Chemistry, Cambridge University, Cambridge, CB2 1EW, UK

SO Biochemistry (1994), 33(25), 7957-63

CODEN: BICHAW; ISSN: 0006-2960

DT Journal

LA English

AB The suitability of the barley chymotrypsin inhibitor-2 for study by fragmentation and complementation has been analyzed. The primary residue for binding to proteases, Met-59 (the unique methionine in

the sequence), lies in a broad, solvent-exposed loop. The bond between

Met-59 and Glu-60 was cleaved by cyanogen bromide. The two fragments thus

obtained, i.e., CI-2(20-59) and CI-2(60-83), associate (KD = 42 nM) to yield

a complex that has fluorescence and CD spectra identical to those of

uncleaved chymotrypsin inhibitor-2. Recovery of native-like structure is

further indicated by the ability of the complex to inhibit chymotrypsin,

although the [I]50% is 140-fold higher than for the uncleaved inhibitor.

CI-2(60-83) appears to be highly disordered in water, but fragment

CI(20-59) forms a significant structure, as judged by its circular

dichroism spectra and evidence from one-dimensional NMR. The CD spectra

of CI-2(20-59) approach the baseline in 4 M guanidinium chloride but

display characteristics of an α -helix in the presence of trifluoroethanol. Anal. ultracentrifugation shows no

concentration-dependent

change in the mol. weight of the monomer of CI-2(20-59). Both one- and

two-dimensional NMR of the complex [CI-2(20-59)·(60-83)] show unequivocally the presence of a folded structure, which appears

to be

slightly different from the uncleaved native protein.